SEQUENCE PROTOCOL

<110> Degussa AG

## 5 <120> Nucleotide sequences which code for the dps gene <130> 000555 BT <140> 10 <141> <160> 4 <170> PatentIn Ver. 2.1 15 <210> 1 <211> 1377 <212> DNA <213> Corynebacterium glutamicum 20 <220> <221> CDS <222> (504)..(998) <223> dps gene 25 <400> 1 gggtgcgctc tgcatcggtg atcaacctgc accattgggg tccgcgcaaa ttagctgcga 60 tctccccgtc ggaaaggtgc aggcgaatct gcccgcgggt ttcttccgca ggttcaaact 120 30 gcaacgtgcc aatcagcccc aaatggatat acaaaatgtg ctcagggtga tccgcatcga 180 actogacqaa caggtgottg cogtaagoot cogcaacogo gatgoggtga cogttgatga 240 35 tegeogette agaagtaaag egteettgag gtgaagtgge gteeaaaatg gtategeeaa 300 aattettggt gagtteecca getagtegat gaateaegtg teetteagge ataateacca 360 accttaqtaq ccqqtqtqcc qatttqataa aaaactaaqc qtqqcctqcq qqaatcqqca 420 40 ctttcaggat aggacaacct aatataaata agcttaggct aagggccggt gacaatttat 480 caagcagtgc tataataggg gtc atg gca aac tac aca gtc cct gga atc aac 533 Met Ala Asn Tyr Thr Val Pro Gly Ile Asn 45 gag aat gac gca aag cag ctt att gat gga ctg cag gag cgt ctc acc 581 Glu Asn Asp Ala Lys Gln Leu Ile Asp Gly Leu Gln Glu Arg Leu Thr 50 gac tac aac gat ctt cac ctc atc ttg aag cac gtg cac tgg aac gtc 629 Asp Tyr Asn Asp Leu His Leu Ile Leu Lys His Val His Trp Asn Val 30 35 55 act ggc ccc aac ttc att gct gtt cac gaa atg ctc gac cca cag gtt 677 Thr Gly Pro Asn Phe Ile Ala Val His Glu Met Leu Asp Pro Gln Val 50 45 55

	gac ctt gtt cgt ggc tat gct gac gaa gtt gca gag cgc att tcc acc 725 Asp Leu Val Arg Gly Tyr Ala Asp Glu Val Ala Glu Arg Ile Ser Thr 60 65 70	;		
5	ctc gga ggc gca cca gtt gga acc cca gaa ggc cac gtt gct gac cgc 773 Leu Gly Gly Ala Pro Val Gly Thr Pro Glu Gly His Val Ala Asp Arg 75 80 85 90	}		
10	acc cca ctg caa tat gag cgc aat gcc gga aat gtc caa gca cac ctc 821 Thr Pro Leu Gln Tyr Glu Arg Asn Ala Gly Asn Val Gln Ala His Leu 95 100 105	L		
15	act gac ctc aat cgc gtg tac acc caa gtg ctg acc gga gtt cgc gag  Thr Asp Leu Asn Arg Val Tyr Thr Gln Val Leu Thr Gly Val Arg Glu  110 115 120	)		
0.0	tcc atg gca tca gcc ggc cca gtg gat cca gta act gaa gac atc tac  Ser Met Ala Ser Ala Gly Pro Val Asp Pro Val Thr Glu Asp Ile Tyr  125  130  135	7		
20	atc agc cag gcc gcg gag ctg gag aaa ttc cag tgg ttc atc cgc gca  11e Ser Gln Ala Ala Glu Leu Glu Lys Phe Gln Trp Phe Ile Arg Ala  140  145	5		
25	cac att gtt gat gta gac gga aac atc caa gag taaaacgtcg aaaagcgtta 101 His Ile Val Asp Val Asp Gly Asn Ile Gln Glu 155 160 165	18		
30	aggcgctgac ccccaccagc ccgggggtca gtggcttcct tagtgcaaaa atccaccaca 107	78		
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55	Leu Ile Leu Lys His Val His Trp Asn Val Thr Gly Pro Asn Phe Ile 35 40 45			
	Ala Val His Glu Met Leu Asp Pro Gln Val Asp Leu Val Arg Gly Tyr 50 55 60			

	65 70 75 80	
5	Gly Thr Pro Glu Gly His Val Ala Asp Arg Thr Pro Leu Gln Tyr Glu 85 90 95	
	Arg Asn Ala Gly Asn Val Gln Ala His Leu Thr Asp Leu Asn Arg Val	
10	Tyr Thr Gln Val Leu Thr Gly Val Arg Glu Ser Met Ala Ser Ala Gly 115 120 125	
15	Pro Val Asp Pro Val Thr Glu Asp Ile Tyr Ile Ser Gln Ala Ala Glu 130 135 140	
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